

Introducción a la filogenómica microbiana – GET_PHYLOMARKERS

**Microbial genome evolution –
Phylogenomics & GET_PHYLOMARKERS**

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**Introducción a la Filoinformática:
Pan-genómica y Filogenómica microbiana –
NNB & CCG-UNAM, 1-5 Agosto 2022**
<https://github.com/vinuesa/TIB-filoinfo>

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Introducción a la filoinformática – pan-genómica y filogenómica microbiana,
TIB2022, 1-5 Agosto, 2022 CCG-UNAM, Cuernavaca, Mor. México
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Frontiers in Microbiology Research Topics

Microbial Taxonomy, Phylogeny and Biodiversity

Submission closed.

GET_PHYLOMARKERS, a Software Package to Select Optimal Orthologous Clusters for Phylogenomics and Inferring Pan-Genome Phylogenies, Used for a Critical Geno-Taxonomic Revision of the Genus Stenotrophomonas

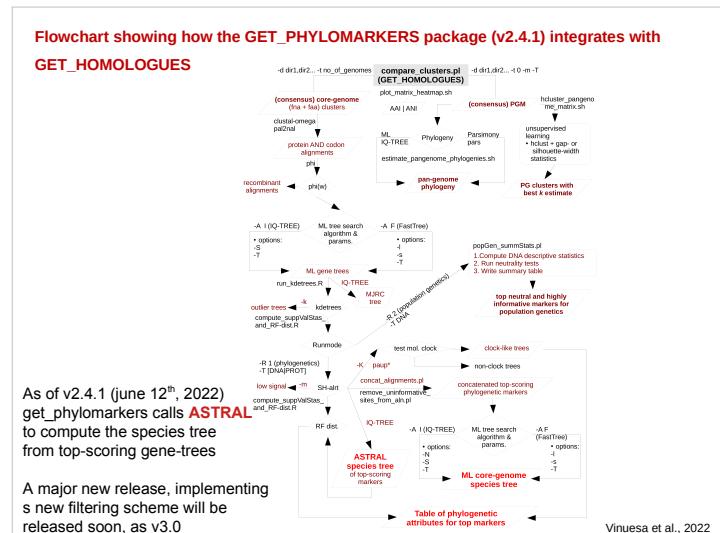
Pablo Vinuesa, Luz E. Ochoa-Sánchez and Bruno Contreras-Moreira

Original Research The massive accumulation of genome-sequences in public databases promoted the proliferation of genome-level phylogenetic analyses in many areas of biological research. However, due to diverse evolutionary and genetic processes, many loci have ...

Published on 01 May 2018
Front. Microbiol. doi: 10.3389/fmicb.2018.00771

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